```
  1 MDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSAN  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 ..PPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSAN  48

 51 YSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPF 100
    |||||||||||||||||||||||||||||||||||||||||||||||||
 49 YSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHILTHTGEKPF  98

101 VCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLK 150
    ||||  |||||||||||||||||||||||||||||||||||||||||||
 99 VCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKTFKKHQQLK 148

151 IHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAK 200
    |||||||||||||||||||||||||||||||||||||||||||||||||
149 IHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQKGCSFVAK 198

201 TWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPR 250
    |||||||||||||||||||||||||||||||||||||||||||||||||
199 TWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPERDVCRCPR 248

251 EGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
249 EGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQSLTRHAVV 298

301 HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNC 350
    |||||||||||||||||||||||||||||||||||||||||||||||||
299 HDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLCQNGESPNC 348

351 VEDKMLSTVAVLTLG 365
    |||||||||||||||
349 VEDKMLSTVAVLTLG 363
```

FIGURE 1

```
  1 ........MDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFIC  42
          :|||||||||||||||||||||||||||||||||||||||||||
 51 PGLGGAGALDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFIC 100

 43 SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL  92
    |||||||||||||||||||||||||||||||||||||||||||||||||
101 SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL 150

 93 THTGEKPFVCAATGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT 142
    |||||||||| ||||||||||||||||||||||||||||||||||||||
151 THTGEKPFVCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT 200

143 FKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ 192
    |||||||||||||.||||||||||||||||||||||||||||||||||||
201 FKKHQQLKIHQCQNTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ 250

193 KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE 242
    |||||||||||||||||||||||||||||||||||||||||||||||||
251 KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE 300

243 RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ 292
    |||||||||||||||||||||||||||||||||||||||||||||||||
301 RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ 350

293 SLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLC 342
    |||||||||||||||||||||||||||||            ||||||||||
351 SLTRHAVVHDPDKKKMKLKVKKSREKREFGLSSQWIYPPKRKQGQGLSLC 400

343 QNGESPNCVEDKMLSTVAVLTLG 365
    |||||||||||||||||||||||
401 QNGESPNCVEDKMLSTVAVLTLG 423
```

FIGURE 2

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```
 51 PGLGGAGALDPPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFIC 100
             |||||||||||||||||||||||||||||||||||||||
  1 ..........PPAVVAESVSSLTIADAFIAAGESSAPTPPRPALPRRFIC  40

101 SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL 150
    |||||||||||||||||||||||||||||||||||||||||||||||||
 41 SFPDCSANYSKAWKLDAHLCKHTGERPFVCDYEGCGKAFIRDYHLSRHIL  90

151 THTGEKPFVCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT 200
    |||||||||||||||||||||||||||||||||||||||||||||||||
 91 THTGEKPFVCAANGCDQKFNTKSNLKKHFERKHENQQKQYICSFEDCKKT 140

201 FKKHQQLKIHQCQNTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ 250
    |||||||||||||||.|||||||||||||||||||||||||||||||||
141 FKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEGYVCQ 190

251 KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
191 KGCSFVAKTWTELLKHVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPE 240

301 RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ 350
    |||||||||||||||||||||||||||||||||||||||||||||||||
241 RDVCRCPREGCGRTYTTVFNLQSHILSFHEESRPFVCEHAGCGKTFAMKQ 290

351 SLTRHAVVHDPDKKKMKLKVKKSREKREFGLSSQWIYPPKRKQGQGLSLC 400
    ||||||||||||||||||||||||||||         |||||||||||||
291 SLTRHAVVHDPDKKKMKLKVKKSREKRSLASHLSGYIPPKRKQGQGLSLC 340

401 QNGESPNCVEDKMLSTVAVLTLG 423
    |||||||||||||||||||||||
341 QNGESPNCVEDKMLSTVAVLTLG 363
```

FIGURE 3

```
  1  CCGCCGGCCGTGGTCGCCGAGTCGGTGTCGTCCTTGACCATCGCCGACGC   50
  1   P  P  A  V  V  A  E  S  V  S  S  L  T  I  A  D  A   17

 51  GTTCATTGCAGCCGGCGAGAGCTCAGCTCCGACCCCGCCGCGCCCCGCGC  100
 18   F  I  A  A  G  E  S  S  A  P  T  P  P  R  P  A  L   34

101  TTCCCAGGAGGTTCATCTGCTCCTTCCCTGACTGCAGCGCCAATTACAGC  150
 35    P  R  R  F  I  C  S  F  P  D  C  S  A  N  Y  S     50

151  AAAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACACGGGGGAGAGACC  200
 51   K  A  W  K  L  D  A  H  L  C  K  H  T  G  E  R  P   67

201  ATTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATCAGGGACTACC  250
 68   F  V  C  D  Y  E  G  C  G  K  A  F  I  R  D  Y  H   84

251  ATCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTTTGTTTGT  300
 85    L  S  R  H  I  L  T  H  T  G  E  K  P  F  V  C    100

301  GCAGCCAATGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAA  350
101   A  A  N  G  C  D  Q  K  F  N  T  K  S  N  L  K  K   117

351  ACATTTTGAACGCAAACATGAAAATCAACAAAAACAATATATATGCAGTT  400
118   H  F  E  R  K  H  E  N  Q  Q  K  Q  Y  I  C  S  F   134

401  TTGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCAT  450
135    E  D  C  K  K  T  F  K  K  H  Q  Q  L  K  I  H    150

451  CAGTGCCAGCATACCAATGAACCTCTATTCAAGTGTACCCAGGAAGGATG  500
151   Q  C  Q  H  T  N  E  P  L  F  K  C  T  Q  E  G  C   167

501  TGGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCC  550
168   G  K  H  F  A  S  P  S  K  L  K  R  H  A  K  A  H   184

551  ACGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGG  600
185    E  G  Y  V  C  Q  K  G  C  S  F  V  A  K  T  W    200

601  ACGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATG  650
201   T  E  L  L  K  H  V  R  E  T  H  K  E  E  I  L  C   217
```

FIGURE 4

```
651  TGAAGTATGCCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACA  700
218    E   V   C   R   K   T   F   K   R   K   D   Y   L   K   Q   H   M  234

701  TGAAAACTCATGCCCCAGAAAGGGATGTATGTCGCTGTCCAAGAGAAGGC  750
235    K   T   H   A   P   E   R   D   V   C   R   C   P   R   E   G  250

751  TGTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATCCTCTC  800
251    C   G   R   Y   T   T   V   F   N   L   Q   S   H   I   L   S  267

801  CTTCCATGAGGAAAGCCGCCCTTTTGTGTGTGAACATGCTGGCTGTGGCA  850
268    F   H   E   E   S   R   P   F   V   C   E   H   A   G   C   G   K  284

851  AAACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGAT  900
285    T   F   A   M   K   Q   S   L   T   R   H   A   V   V   H   D  300

901  CCTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACG  950
301    P   D   K   K   K   M   K   L   K   V   K   K   S   R   E   K   R  317

951  GAGTTTGGCCTCTCATCTCAGTGGATATATCCCTCCCAAAAGGAAACAAG  1000
318    S   L   A   S   H   L   S   G   Y   I   P   P   K   R   K   Q   G  334

1001 GGCAAGGCTTATCTTTGTGTCAAAACGGAGAGTCACCCAACTGTGTGGAA  1050
335    Q   G   L   S   L   C   Q   N   G   E   S   P   N   C   V   E  350

1051 GACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAAGAACTGCA  1100
351    D   K   M   L   S   T   V   A   V   L   T   L   G   *  364

1101 CTGCTTTGTTTAAAGGACTGCAGACCAAGGAGCGAGCTTTCTCTCAGAGC  1150

1151    ATGCTTTTCTTTATTAAAATTAC  1173
```

FIGURE 4

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```
  1  ATGCGCGATCTCCCGGAGCATGCGCAGCAGCGGCGCCGACGCGGGGCGGT   50
  1                   M  R  S  S  G  A  D  A  G  R  C    11

 51  GCCTGGTGACCGCGCGCGCTCCCGGAAGTGTGCCGGCGTCGCGCGAAGGT  100
 12   L  V  T  A  R  A  P  G  S  V  P  A  S  R  E  G     27

101  TCAGCAGGGAGCCGTGGGCCGGGCGCGCGGTTCCCGGCACGTGTCTCGGC  150
 28   S  A  G  S  R  G  P  G  A  R  F  P  A  R  V  S  A  44

151  ACGTGGCAGCGCGCCTGGCCCTGGGCTTGGAGGCGCCGGCGCCCTGGATC  200
 45   R  G  S  A  P  G  P  G  L  G  G  A  G  A  L  D  P  61

201  CGCCGGCCGTGGTCGCCGAGTCGGTGTCGTCCTTGACCATCGCCGACGCG  250
 62    P  A  V  V  A  E  S  V  S  S  L  T  I  A  D  A    77

251  TTCATTGCAGCCGGCGAGAGCTCAGCTCCGACCCCGCCGCGCCCCGCGCT  300
 78   F  I  A  A  G  E  S  S  A  P  T  P  P  R  P  A  L  94

301  TCCCAGGAGGTTCATCTGCTCCTTCCCTGACTGCAGCGCCAATTACAGCA  350
 95   P  R  R  F  I  C  S  F  P  D  C  S  A  N  Y  S  K  111

351  AAGCCTGGAAGCTTGACGCGCACCTGTGCAAGCACACGGGGGAGAGACCA  400
112    A  W  K  L  D  A  H  L  C  K  H  T  G  E  R  P    127

401  TTTGTTTGTGACTATGAAGGGTGTGGCAAGGCCTTCATCAGGGACTACCA  450
128   F  V  C  D  Y  E  G  C  G  K  A  F  I  R  D  Y  H  144

451  TCTGAGCCGCCACATTCTGACTCACACAGGAGAAAAGCCGTTTGTTTGTG  500
145   L  S  R  H  I  L  T  H  T  G  E  K  P  F  V  C  A  161

501  CAGCCAATGGCTGTGATCAAAAATTCAACACAAAATCAAACTTGAAGAAA  550
162    A  N  G  C  D  Q  K  F  N  T  K  S  N  L  K  K    177₁

551  CATTTTGAACGCAAACATGAAAATCAACAAAAACAATATATATGCAGTTT  600
178   H  F  E  R  K  H  E  N  Q  Q  K  Q  Y  I  C  S  F  194

601  TGAAGACTGTAAGAAGACCTTTAAGAAACATCAGCAGCTGAAAATCCATC  650
195   E  D  C  K  K  T  F  K  K  H  Q  Q  L  K  I  H  Q  211

651  AGTGCCAGAATACCAATGAACCTCTATTCAAGTGTACCCAGGAAGGATGT  700
212   C  Q  N  T  N  E  P  L  F  K  C  T  Q  E  G  C     227
```

FIGURE 5

```
 701  GGGAAACACTTTGCATCACCCAGCAAGCTGAAACGACATGCCAAGGCCCA   750
 228   G   K   H   F   A   S   P   S   K   L   K   R   H   A   K   A   H    244


 751  CGAGGGCTATGTATGTCAAAAAGGATGTTCCTTTGTGGCAAAAACATGGA   800
 245   E   G   Y   V   C   Q   K   G   C   S   F   V   A   K   T   W   T    261


 801  CGGAACTTCTGAAACATGTGAGAGAAACCCATAAAGAGGAAATACTATGT   850
 262    E   L   L   K   H   V   R   E   T   H   K   E   E   I   L   C      277


 851  GAAGTATGCCGGAAAACATTTAAACGCAAAGATTACCTTAAGCAACACAT   900
 278   ·E   V   C   R   K   T   F   K   R   K   D   Y   L   K   Q   H   M   294


 901  GAAAACTCATGCCCCAGAAAGGGATGTATGTCGCTGTCCAAGAGAAGGCT   950
 295   K   T   H   A   P   E   R   D   V   C   R   C   P   R   E   G   C    311


 951  GTGGAAGAACCTATACAACTGTGTTTAATCTCCAAAGCCATATCCTCTCC  1000
 312    G   R   T   Y   T   T   V   F   N   L   Q   S   H   I   L   S      327


1001  TTCCATGAGGAAAGCCGCCCTTTTGTGTGTGAACATGCTGGCTGTGGCAA  1050
 328   F   H   E   E   S   R·  P   F   V   C   E   H   A   G   C   G   K    344


1051  AACATTTGCAATGAAACAAAGTCTCACTAGGCATGCTGTTGTACATGATC  1100
 345   T   F   A   M   K   Q   S   L   T   R   H   A   V   V   H   D   P    361


1101  CTGACAAGAAGAAAATGAAGCTCAAAGTCAAAAAATCTCGTGAAAAACGG  1150
 362    D   K   K   K   M   K   L   K   V   K   K   S   R   E   K   R      377


1151  GAGTTTGGCCTCTCATCTCAGTGGATATATCCTCCCAAAAGGAAACAAGG  1200
 378   E   F   G   L   S   S   Q   W   I   Y   P   P   K   R   K   Q   G    394


1201  GCAAGGCTTATCTTTGTGTCAAAACGGAGAGTCACCCAACTGTGTGGAAG  1250
 395   Q   G   L   S   L   C   Q   N   G   E   S   P   N   C   V   E   D   411ₗ


1251  ACAAGATGCTCTCGACAGTTGCAGTACTTACCCTTGGCTAAGAACTGCAC  1300
 412    K   M   L   S   T   V   A   V   L   T   L   G   *                 424


1301  TGCTTTGTTTAAAGGACTGCAGACCAAGGAGTCGAGCTTTCTCTCAGAGC  1350


ATGCTTTTCTTTATTAAAATTACTGATGCAGAAAAAAAAAAAAAAAAAA         1399
```

FIGURE 5